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TECH CENTER 1600/2900



1632

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/754,997A

DATE: 02/13/2002

TIME: 15:28:10

Input Set : A:\NI4552.txt

Output Set: N:\CRF3\02132002\I754997A.raw

ENTERED

4 <110> APPLICANT: Salbaum, Michael J.
 6 <120> TITLE OF INVENTION: NOPE Polypeptides, Encoding Nucleic
 7 Acids and Methods of Use
 9 <130> FILE REFERENCE: P-NI 4552
 11 <140> CURRENT APPLICATION NUMBER: US 09/754,997A
 12 <141> CURRENT FILING DATE: 2001-01-04
 14 <150> PRIOR APPLICATION NUMBER: US 60/174,496
 15 <151> PRIOR FILING DATE: 2000-01-04
 17 <150> PRIOR APPLICATION NUMBER: US 60/205,789
 18 <151> PRIOR FILING DATE: 2000-05-19
 20 <160> NUMBER OF SEQ ID NOS: 45
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 6176
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Mus musculus
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)...(3756)
 33 <400> SEQUENCE: 1
 34 atg gcg cgg gcg gac acg ggc cgc ggg ctc ctg gtg ctg acc ttc tgc 48
 35 Met Ala Arg Ala Asp Thr Gly Arg Gly Leu Leu Val Leu Thr Phe Cys
 36 1 5 10 15
 38 ctg ctg tcc gcg cgc ggg gag ctg cca ttg ccc cag gag aca act gtc 96
 39 Leu Leu Ser Ala Arg Gly Glu Leu Pro Leu Pro Gln Glu Thr Thr Val
 40 20 25 30
 42 aag ctg agc tgt gat gag gga ccc ctg caa gtg atc ctg ggc cct gag 144
 43 Lys Leu Ser Cys Asp Glu Gly Pro Leu Gln Val Ile Leu Gly Pro Glu
 44 35 40 45
 46 cag gct gtg gtg ctg gac tgc act ttg ggg gct aca gct gct ggg cct 192
 47 Gln Ala Val Val Leu Asp Cys Thr Leu Gly Ala Thr Ala Ala Gly Pro
 48 50 55 60
 50 ccg acc agg gtg aca tgg agc aag gat gga gac act gta cta gag cat 240
 51 Pro Thr Arg Val Thr Trp Ser Lys Asp Gly Asp Thr Val Leu Glu His
 52 65 70 75 80
 54 gag aac ctg cac ctg cta ccc aat ggc tcc ctg tgg ctg tcc tca ccc 288
 55 Glu Asn Leu His Leu Leu Pro Asn Gly Ser Leu Trp Leu Ser Ser Pro
 56 85 90 95
 58 cta gag caa gaa gac agc gat gat gag gaa gct ctt agg atc tgg aag 336
 59 Leu Glu Gln Glu Asp Ser Asp Asp Glu Glu Ala Leu Arg Ile Trp Lys
 60 100 105 110
 62 gtc act gag ggc agc tat tcc tgt ctg gcc cac agc ccg cta gga gtg 384
 63 Val Thr Glu Gly Ser Tyr Ser Cys Leu Ala His Ser Pro Leu Gly Val

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64	115	120	125														
66	gtg	gcc	agc	cag	gtt	gct	gtg	gtc	aag	ctt	gcc	aca	ctc	gaa	gac	ttc	432
67	Val	Ala	Ser	Gln	Val	Ala	Val	Val	Lys	Leu	Ala	Thr	Leu	Glu	Asp	Phe	
68	130						135					140					
70	tct	ctg	cac	ccc	gag	tcc	cag	att	gtg	gag	gag	aac	ggg	aca	gca	cgc	480
71	Ser	Leu	His	Pro	Glu	Ser	Gln	Ile	Val	Glu	Glu	Asn	Gly	Thr	Ala	Arg	
72	145						150					155				160	
74	ttt	gaa	tgc	cac	acc	aag	ggc	ctt	cca	gcc	ccc	atc	att	act	tgg	gaa	528
75	Phe	Glu	Cys	His	Thr	Lys	Gly	Leu	Pro	Ala	Pro	Ile	Ile	Thr	Trp	Glu	
76							165					170			175		
78	aag	gac	cag	gtg	acc	gtg	cct	gag	gag	ccc	cgg	ctc	atc	act	ctt	ccc	576
79	Lys	Asp	Gln	Val	Thr	Val	Pro	Glu	Glu	Pro	Arg	Leu	Ile	Thr	Leu	Pro	
80							180					185			190		
82	aag	tgg	ctc	ctc	cag	atc	cta	gat	gtc	cag	agt	gat	gca	ggc	tcc	624	
83	Lys	Trp	Leu	Leu	Gln	Ile	Leu	Asp	Val	Gln	Asp	Ser	Asp	Ala	Gly	Ser	
84							195					200			205		
86	tac	cgc	tgc	gtg	gcc	acc	aat	tca	gcc	cgc	caa	cga	ttc	agc	cag	gag	672
87	Tyr	Arg	Cys	Val	Ala	Thr	Asn	Ser	Ala	Arg	Gln	Arg	Phe	Ser	Gln	Glu	
88							210					215			220		
90	gcc	tgc	ctc	act	gtg	gcc	ctc	aga	ggg	tct	ttg	gag	gct	acc	agg	ggg	720
91	Ala	Ser	Leu	Thr	Val	Ala	Leu	Arg	Gly	Ser	Leu	Glu	Ala	Thr	Arg	Gly	
92	225						230					235			240		
94	cag	gat	gtg	gtc	att	gtg	gca	gcc	cca	gag	aac	acc	acg	gta	gtg	tct	768
95	Gln	Asp	Val	Val	Ile	Val	Ala	Ala	Pro	Glu	Asn	Thr	Thr	Val	Val	Ser	
96							245					250			255		
98	gga	cag	aat	gta	gtg	atg	gag	tgc	gtg	gcc	tct	gct	gac	ccc	acc	cct	816
99	Gly	Gln	Asn	Val	Val	Met	Glu	Cys	Val	Ala	Ser	Ala	Asp	Pro	Thr	Pro	
100							260					265			270		
102	ttt	gtg	tcc	tgg	gtc	cga	cag	gat	gga	aag	cct	atc	tcc	acg	gtc	864	
103	Phe	Val	Ser	Trp	Val	Arg	Gln	Asp	Gly	Lys	Pro	Ile	Ser	Thr	Asp	Val	
104							275					280			285		
106	atc	gtt	ctg	ggc	cg	acc	aat	cta	ctc	atc	gcc	agc	g	c	cg	912	
107	Ile	Val	Leu	Gly	Arg	Thr	Asn	Leu	Leu	Ile	Ala	Ser	Ala	Gln	Pro	Arg	
108							290					295			300		
110	cac	tct	gga	gtc	tat	gtc	tgc	cga	gcc	aac	gg	ccc	ctc	acg	cgt	gac	960
111	His	Ser	Gly	Val	Tyr	Val	Cys	Arg	Ala	Asn	Lys	Pro	Leu	Thr	Arg	Asp	
112	305						310					315			320		
114	ttc	gcc	act	g	cg	g	c	t	g	a	c	t	g	cc	cc	atc	1008
115	Phe	Ala	Thr	Ala	Ala	Ala	Glu	Leu	Arg	Val	Leu	Ala	Ala	Pro	Ala	Ile	
116							325					330			335		
118	tcg	cag	gca	ccc	gag	g	cg	ctc	cg	ac	cg	gg	cc	ac	gc	cg	1056
119	Ser	Gln	Ala	Pro	Glu	Ala	Leu	Ser	Arg	Thr	Arg	Ala	Ser	Thr	Ala	Arg	
120							340					345			350		
122	ttc	gtg	tgc	cg	gg	g	gg	cca	cg	cc	cg	ctg	cac	tgg	ctg	1104	
123	Phe	Val	Cys	Arg	Ala	Ser	Gly	Glu	Pro	Arg	Pro	Ala	Leu	His	Trp	Leu	
124							355					360			365		
126	cac	gac	ggg	atc	ccg	ttg	cga	ccc	aat	ggg	cg	gc	gt	cag	gg	1152	
127	His	Asp	Gly	Ile	Pro	Leu	Arg	Pro	Asn	Gly	Arg	Val	Lys	Val	Gln	Gly	
128							370					375			380		

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130	ggc ggc ggc agc ttg gtc atc act cag atc ggc ctg cag gac gct ggc	1200
131	Gly Gly Gly Ser Leu Val Ile Thr Gln Ile Gly Leu Gln Asp Ala Gly	
132	385 390 395 400	1248
134	tac tac cag tgc gta gca gaa aac agc gcg gga act gcc tgt gcc gct	
135	Tyr Tyr Gln Cys Val Ala Glu Asn Ser Ala Gly Thr Ala Cys Ala Ala	
136	405 410 415 420 425 430	1296
138	gct ccc ctg gcg gta gtg gtg cgc gag ggg ctg ccc agc gcc ccg act	
139	Ala Pro Leu Ala Val Val Val Arg Glu Gly Leu Pro Ser Ala Pro Thr	
140	420 425 430 435 440 445	1344
142	cgg gtc aca gcc acg ccg ctg agc agc tcc tct gtg ctg gtg gcc tgg	
143	Arg Val Thr Ala Thr Pro Leu Ser Ser Ser Val Leu Val Ala Trp	
144	435 440 445 450 455 460	1392
146	gag cgg cct gag ttg cac agc gag caa atc att ggc ttc tct ctt cac	
147	Glu Arg Pro Glu Leu His Ser Glu Gln Ile Ile Gly Phe Ser Leu His	
148	450 455 460 465 470 475	1440
150	tac caa aag gca agg gga gtg gac aat gtg gag tac cag ttt gca gta	
151	Tyr Gln Lys Ala Arg Gly Val Asp Asn Val Glu Tyr Gln Phe Ala Val	
152	465 470 475 480 485 490	1488
154	aac aat gac acc aca gag ctg cag gtt cgg gac ctg gaa ccc aac acg	
155	Asn Asn Asp Thr Thr Glu Leu Gln Val Arg Asp Leu Glu Pro Asn Thr	
156	485 490 495 500 505 510	1536
158	gat tat gag ttc tac gtg gtg gcc tac tcc cag ctg ggg gcc agc cga	
159	Asp Tyr Glu Phe Tyr Val Val Ala Tyr Ser Gln Leu Gly Ala Ser Arg	
160	500 505 510 515 520 525	1584
162	acc tcc agc cca gcc ctg gtg cat aca ctg gac gat gtc ccc agc gca	
163	Thr Ser Ser Pro Ala Leu Val His Thr Leu Asp Asp Val Pro Ser Ala	
164	515 520 525 530 535 540	1632
166	gca ccc cag ctt acc ttg tcc agc ccc aac ccc tcg gac atc agg gtg	
167	Ala Pro Gln Leu Thr Leu Ser Ser Pro Asn Pro Ser Asp Ile Arg Val	
168	530 535 540 545 550 555	1680
170	gca tgg ctg ccc ctg ccc tcc agc ctg agc aat gga cag gtg ctg aag	
171	Ala Trp Leu Pro Leu Pro Ser Ser Leu Ser Asn Gly Gln Val Leu Lys	
172	545 550 555 560 565 570	1728
174	tac aag ata gag tac ggt ttg ggg aag gaa gat cag gtt ttc tcc acc	
175	Tyr Lys Ile Glu Tyr Gly Leu Gly Lys Glu Asp Gln Val Phe Ser Thr	
176	565 570 575 580 585 590	1776
178	gag gtg cct gga aat gag aca caa ctt acg tta aac tca ctt cag cca	
179	Glu Val Pro Gly Asn Glu Thr Gln Leu Thr Leu Asn Ser Leu Gln Pro	
180	580 585 590 595 600 605	1824
182	aac aaa gtg tac cga gtc cgg att tca gct ggc act ggc gct ggc tat	
183	Asn Lys Val Tyr Arg Val Arg Ile Ser Ala Gly Thr Gly Ala Gly Tyr	
184	595 600 605 610 615 620	1872
186	gga gtc cct tct cag tgg atg cag cac agg aca cct ggt gtg cac aac	
187	Gly Val Pro Ser Gln Trp Met Gln His Arg Thr Pro Gly Val His Asn	
188	610 615 620 625 630 635	1920
190	cag agc cat gtt ccc ttt gcc cct gca gaa ttg aag gtg agg gca aag	
191	Gln Ser His Val Pro Phe Ala Pro Ala Glu Leu Lys Val Arg Ala Lys	
192	625 630 635 640 645 650	1968
194	atg gag tcc ctg gtg tca tgg cag ccg ccc cct cac ccc acc cag	

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195	Met	Glu	Ser	Leu	Val	Val	Ser	Trp	Gln	Pro	Pro	Pro	His	Pro	Thr	Gln	
196		645							650						655		
198	atc	tct	gga	tac	aaa	ctc	tac	tgg	gga	gag	gtg	gga	aca	gag	gag	gag	2016
199	Ile	Ser	Gly	Tyr	Lys	Leu	Tyr	Trp	Gly	Glu	Val	Gly	Thr	Glu	Glu	Glu	
200						660				665				670			
202	gca	gat	ggt	gac	cgc	ccc	cca	ggg	ggt	cgt	gga	gat	caa	gct	tgg	gac	2064
203	Ala	Asp	Gly	Asp	Arg	Pro	Pro	Gly	Gly	Arg	Gly	Asp	Gln	Ala	Trp	Asp	
204						675				680				685			
206	gtc	ggg	ccc	gtg	cgg	ctg	aag	aag	aaa	gtg	aag	cag	tat	gaa	ctg	acc	2112
207	Val	Gly	Pro	Val	Arg	Leu	Lys	Lys	Lys	Val	Lys	Gln	Tyr	Glu	Leu	Thr	
208						690				695				700			
210	cag	tta	gtc	cct	ggc	agg	ccg	tac	gag	gtg	aag	ctc	gta	gct	ttc	aac	2160
211	Gln	Leu	Val	Pro	Gly	Arg	Pro	Tyr	Glu	Val	Lys	Leu	Val	Ala	Phe	Asn	
212						705				710				715		720	
214	aaa	cac	gag	gac	gac	tac	gct	gct	gtg	tgg	aag	ggc	aag	acg	gag	aag	2208
215	Lys	His	Glu	Asp	Gly	Tyr	Ala	Ala	Val	Trp	Lys	Gly	Lys	Thr	Glu	Lys	
216						725					730				735		
218	gcg	ccc	acg	cca	gac	ctg	cct	atc	cag	agg	ggg	cca	ccg	ctg	cct	cct	2256
219	Ala	Pro	Thr	Pro	Asp	Leu	Pro	Ile	Gln	Arg	Gly	Pro	Pro	Leu	Pro	Pro	
220						740				745				750			
222	gcc	cat	gtc	cac	gca	gag	tca	aac	agc	tcc	act	tcc	att	tgg	ctt	cg	2304
223	Ala	His	Val	His	Ala	Glu	Ser	Asn	Ser	Ser	Thr	Ser	Ile	Trp	Leu	Arg	
224						755				760				765			
226	tgg	aag	aag	cca	gac	ttt	acc	act	gtc	aag	att	gtc	aac	tac	act	gta	2352
227	Trp	Lys	Lys	Pro	Asp	Phe	Thr	Thr	Val	Lys	Ile	Val	Asn	Tyr	Thr	Val	
228						770				775				780			
230	cgc	ttc	ggc	ccc	tgg	ggg	ctc	agg	aat	gct	tcc	ctg	gtc	acc	tac	tat	2400
231	Arg	Phe	Gly	Pro	Trp	Gly	Leu	Arg	Asn	Ala	Ser	Leu	Val	Thr	Tyr	Tyr	
232						785				790				795		800	
234	acc	agc	tct	gga	gaa	gac	att	ctc	att	ggc	ggc	ctg	aaa	cca	ttt	acc	2448
235	Thr	Ser	Ser	Gly	Glu	Asp	Ile	Leu	Ile	Gly	Gly	Leu	Lys	Pro	Phe	Thr	
236						805					810				815		
238	aag	tac	gag	ttt	gct	gta	cag	tcc	cac	gga	gtg	gat	atg	gat	ggg	ccc	2496
239	Lys	Tyr	Glu	Phe	Ala	Val	Gln	Ser	His	Gly	Val	Asp	Met	Asp	Gly	Pro	
240						820				825				830			
242	ttt	ggc	tcc	gtc	gta	gaa	cg	cc	tt	ctg	cc	g	cc	c	tca	aca	2544
243	Phe	Gly	Ser	Val	Val	Glu	Arg	Ser	Thr	Leu	Pro	Asp	Arg	Pro	Ser	Thr	
244						835				840				845			
246	cct	cct	tct	gac	ctg	cg	cc	cc	ctg	aca	cc	tcc	acc	gtt	cg	2592	
247	Pro	Pro	Ser	Asp	Leu	Arg	Leu	Ser	Pro	Leu	Thr	Pro	Ser	Thr	Val	Arg	
248						850				855				860			
250	tta	cac	tgg	tgt	ccc	ccc	acg	gag	ccc	aat	ggt	gag	att	gtg	gag	tat	2640
251	Leu	His	Trp	Cys	Pro	Pro	Thr	Glu	Pro	Asn	Gly	Glu	Ile	Val	Glu	Tyr	
252						865				870				875		880	
254	cta	att	ctc	tac	agc	aa	ac	cc	cag	ccc	gaa	cac	cag	tgg	aca		2688
255	Leu	Ile	Leu	Tyr	Ser	Asn	Asn	His	Thr	Gln	Pro	Glu	His	Gln	Trp	Thr	
256						885				890				895			
258	ctg	ctc	acc	aca	gag	gga	aa	atc	tcc	agt	gca	gag	gtc	cat	ggc	cta	2736
259	Leu	Leu	Thr	Thr	Glu	Gly	Asn	Ile	Phe	Ser	Ala	Glu	Val	His	Gly	Leu	

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260	900	905	910	
262	gag agt gac act cgg tat ttc ttc aag atg gga gcc cgc aca gag gtg			2784
263	Glu Ser Asp Thr Arg Tyr Phe Phe Lys Met Gly Ala Arg Thr Glu Val			
264	915	920	925	
266	ggg cct ggg ccc ttt tcc cgc ttg cag gat gtg att act ctg caa gag			2832
267	Gly Pro Gly Pro Phe Ser Arg Leu Gln Asp Val Ile Thr Leu Gln Glu			
268	930	935	940	
270	aca ttc tca gac tcc ttg gat gtg cac gcc gtc acg ggc atc atc gtg			2880
271	Thr Phe Ser Asp Ser Leu Asp Val His Ala Val Thr Gly Ile Ile Val			
272	945	950	955	960
274	gtt gtc tgc ctg ggc ctt ctc tgc ctc ctg gcc tgc atg tgt gct ggc			2928
275	Gly Val Cys Leu Gly Leu Leu Cys Leu Ala Cys Met Cys Ala Gly			
276	965	970	975	
278	cta cga caa agc tcc cac agg gaa gcc ctt ccc gga ttg tcc tcc tca			2976
279	Leu Arg Gln Ser Ser His Arg Glu Ala Leu Pro Gly Leu Ser Ser Ser			
280	980	985	990	
282	ggc acc cca gga aac cca gcg ctc tac aca aga gct cgg ctt ggg cct			3024
283	Gly Thr Pro Gly Asn Pro Ala Leu Tyr Thr Arg Ala Arg Leu Gly Pro			
284	995	1000	1005	
286	ccc agt gtc cct gct gcc cat gag ttg gag tcc ctc gtg cat cct cgt			3072
287	Pro Ser Val Pro Ala Ala His Glu Leu Glu Ser Leu Val His Pro Arg			
288	1010	1015	1020	
290	ccc cag gat tgg tcc cca cca ccc tca gat gtg gaa gac aag gct gaa			3120
291	Pro Gln Asp Trp Ser Pro Pro Pro Ser Asp Val Glu Asp Lys Ala Glu			
292	1025	1030	1035	1040
294	gta cac agc ctt atg ggt ggc agt gtt tca gat tgc cgg ggc cac tcc			3168
295	Val His Ser Leu Met Gly Gly Ser Val Ser Asp Cys Arg Gly His Ser			
296	1045	1050	1055	
298	aag aga aag atc tcc tgg gct cag gca ggg gga cca aac tgg gca ggc			3216
299	Lys Arg Lys Ile Ser Trp Ala Gln Ala Gly Gly Pro Asn Trp Ala Gly			
300	1060	1065	1070	
302	tcc tgg gca ggc tgt gag ctg ccc cag ggt agt ggt cca agg ccg gct			3264
303	Ser Trp Ala Gly Cys Glu Leu Pro Gln Gly Ser Gly Pro Arg Pro Ala			
304	1075	1080	1085	
306	ctg acc cgt gct ctg ctg cct cca gcg gga acc ggg cag aca ctg ctg			3312
307	Leu Thr Arg Ala Leu Leu Pro Pro Ala Gly Thr Gly Gln Thr Leu Leu			
308	1090	1095	1100	
310	ctg caa gcc ctg gtg tat gac ggc ata aag agc aac ggg aga aag aag			3360
311	Leu Gln Ala Leu Val Tyr Asp Gly Ile Lys Ser Asn Gly Arg Lys Lys			
312	1105	1110	1115	1120
314	ccg tcc cca gcc tgc agg aat cag gtg gaa gct gag gtc att gtc cac			3408
315	Pro Ser Pro Ala Cys Arg Asn Gln Val Glu Ala Glu Val Ile Val His			
316	1125	1130	1135	
318	tcc gac ttc ggt gca tcc aaa gga tgt cct gac ctc cac ctc caa gac			3456
319	Ser Asp Phe Gly Ala Ser Lys Gly Cys Pro Asp Leu His Leu Gln Asp			
320	1140	1145	1150	
322	ctg gag cca gag gaa cca ctg act gca gag act ctg cct tcc acg tct			3504
323	Leu Glu Pro Glu Glu Pro Leu Thr Ala Glu Thr Leu Pro Ser Thr Ser			
324	1155	1160	1165	

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